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The MNIST database is a well-known database of handwritten digit images (0-9) that is used to evaluate
machine learning algorithms. The database contains 60,000 training images and 10,000 test images.
The MNIST data is stored in 4 binary files, which can be difficult to manage directly. Download the data
(directly on Yann LeCun's website here or here for Fashion-MNIST) and you can use the code below to
load them under R. In python, they (MNIST and FMNIST) are accessible via the tensorflow API for
example.
 rm(list = ls())
 library(foreach)
 library(doParallel)
 ## Ładowanie wymaganego pakietu: iterators
 ## Ładowanie wymaganego pakietu: parallel
 library(stringr)
 library(e1071)
 library(ggplot2)
 setwd("C:/Machine_Learning_A/Final_Project")
 nTrain <- readBin(con = "train-images.idx3-ubyte", what = "integer", n = 4,
                   size = 4, endian = "big")[2]
 nTest <- readBin(con = "t10k-images.idx3-ubyte", what = "integer", n = 4,
                  size = 4, endian = "big")[2]
 nRows <- readBin(con = "train-images.idx3-ubyte", what = "integer", n = 4,
                  size = 4, endian = "big")[3]
 nCols <- readBin(con = "train-images.idx3-ubyte", what = "integer", n = 4,
                  size = 4, endian = "big")[4]
 # Load training data
 images.train <- array(as.numeric(readBin(con = "train-images.idx3-ubyte",</pre>
                                          what = "raw",
                                         n = nTrain * nRows * nCols + 16,
                                         endian = "big")[-(1:16)]),
                       dim = c(nCols, nRows, nTrain))
 labels.train <- as.numeric(readBin(con = "train-labels.idx1-ubyte",</pre>
                                   what = "raw",
                                   n = nTrain + 8,
                                   endian = "big")[-(1:8)])
 # Load test data
 images.test <- array(as.numeric(readBin(con = "t10k-images.idx3-ubyte",</pre>
                                        what = "raw",
                                        n = nTest * nRows * nCols + 16,
                                        endian = "big")[-(1:16)]),
                      dim = c(nCols, nRows, nTest))
 labels.test <- as.numeric(readBin(con = "t10k-labels.idx1-ubyte",</pre>
                                  what = "raw",
                                  n = nTest + 8,
                                  endian = "big")[-(1:8)])
0. Definitions of function used later on:
 set.seed(12)
 #Functions dataPrep and createMatrix are used to manipulate data (sample etc.)
 dataPrep <- function(p, n, Data_Images, Data_Labels){ #p is portion of Data to keep, n is the pa
 rameter which indicates which
                                                      #labels to keep
   sample_size <- length(Data_Images[1,1,]) * p</pre>
   small_sample <- sample(length(Data_Images[1, 1, ]),</pre>
                          size = sample_size)
   Images <- Data_Images[,,small_sample]</pre>
   Labels <- Data_Labels[small_sample]</pre>
   subs_train <- which(Labels <= n) #Choosing data which has label 0 1 or 2</pre>
   Images <- Images[,,subs_train]</pre>
   Labels <- Labels[subs_train]</pre>
   ret_list <- list(Images, Labels)</pre>
   return(ret_list) #Return is an array with first element with Images and the second with Labels
 createMatrix <- function(Data_List){</pre>
   MatrixTrain <- matrix(0, nrow = length(Data_List[[1]][1,1,]),</pre>
                        ncol = length(c(Data_List[[1]][,,1])))
   for(j in 1:length(Data_List[[1]][1, 1, ])){
     MatrixTrain[j,] <- c(Data_List[[1]][, , j])</pre>
   Matrix_Train <- MatrixTrain/255</pre>
   Labels_Train <- as.factor(Data_List[[2]])</pre>
   ret_list <- list(Matrix_Train, Labels_Train)</pre>
   return(ret_list)
 #Functions fitAndTest and benchmarkValues are used to compare different parameters of a models.
 fitAndTest <- function(train_data, test_data, cost_in = 1, gamma_in = 0.05){</pre>
   svm_fit <- e1071::svm(train_data[[1]],</pre>
                         train_data[[2]],
                         kernel = "radial",
                         cost = cost_in,
                         gamma = gamma_in,
                         scale = TRUE)
   ypred <- predict(svm_fit, test_data[[1]])</pre>
   conf_mat <- table(predict = ypred, truth = test_data[[2]])</pre>
   corr_pred <- 0
   incorr_pred <- 0</pre>
   for(i in 1:ncol(conf_mat)){
     for(j in 1:ncol(conf_mat)){
       if(j == i){
         corr_pred <- corr_pred + conf_mat[i,j]</pre>
       }
       else
         incorr_pred <- incorr_pred + conf_mat[i,j]</pre>
   Total_MissClass_Rate <- corr_pred/(corr_pred + incorr_pred)</pre>
   return(Total_MissClass_Rate)
 benchmarkValues <- function(Data_Imag_Train, Data_Lab_Train, Data_Imag_Test, Data_Lab_Test, n){</pre>
   #n is the number of labels we are considering
   #(e.g. 0, 1, 2 -> n=2)
   MissClassVector <- vector(mode = "double", length = n)</pre>
   sample_Train_inc <- ((1/2)-(1/30))/8
   sample_Test_inc <- ((1/2)-(1/10))/8
   for(i in 2:n){
     p_train <- 1/30 + sample_Train_inc * (i-2)</pre>
     Train_Prep <- dataPrep(p_train, i, Data_Imag_Train, Data_Lab_Train)</pre>
     Train_Data <- createMatrix(Train_Prep)</pre>
     p_test <- 1/10 + sample_Test_inc * (i-2)</pre>
     Test_Prep <- dataPrep(p_test, i, Data_Imag_Test, Data_Lab_Test)</pre>
     Test_Data <- createMatrix(Test_Prep)</pre>
     MissClassVector[i] <- fitAndTest(Train_Data, Test_Data)</pre>
   return(MissClassVector)
1. Display the first 10 images of the training base. You can use the
functions image and grey or the pacakge imager (by converting
them as cimg objects). With Python matplotlib.
 par(mfrow = c(3, 3))
 v <- c(1:28) # We use v to inverse the order of the rows (so that images are familiar to humans)
 for(i in 1:9){
   image(images.train[, , i][, rev(v)], col = grey.colors(n = 255, rev = TRUE))
     0.0 0.2 0.4 0.6 0.8 1.0
     0.0 0.2 0.4 0.6 0.8 1.0
                                                          0.0 0.2 0.4 0.6 0.8 1.0
2. Same question for the first 10 images of the test base
 par(mfrow = c(3, 3))
 for(i in 1:9){
   image(images.test[,,i][, rev(v)], col = grey.colors(n = 255, rev = TRUE))
     0.0 0.2 0.4 0.6 0.8 1.0
                                                          0.0 0.2 0.4 0.6 0.8 1.0
                               0.0 0.2 0.4 0.6 0.8 1.0
3. First, reduce the size of the database (for reasons of
computation time). Create a random subset of the training base of
30 times smaller size. We also restrict ourselves to 3 classes
(0,1,2).
 Train_Prep <- dataPrep(1/30, 2, images.train, labels.train)</pre>
4. Prepare the data for SVM (normalize them). For example, you
can put the training data in a matrix (of suitable size).
 Train_Data <- createMatrix(Train_Prep)</pre>
5. Train an SVM on the training data (e.g. you can use the svm
function from the e1071 package under R, sklearn.svm.SVC
under python). Again, for CPU time reasons, we set the
parameters a priori at first. Use a gaussian kernel K(u,v)
 svm_fit <- e1071::svm(Train_Data[[1]],</pre>
                      Train_Data[[2]],
                       kernel = "radial",
                       cost = 1,
                       gamma = 0.05,
                       scale = TRUE)
6. Reduce the size of the test data (e.g., keep only the first 1000
images) and prepare them in the same way as the training data.
 Test_Prep <- dataPrep(0.1, 2, images.test, labels.test)</pre>
 Test_Data <- createMatrix(Test_Prep)</pre>
7. Calculate the prediction error of the svm (on the first three
classes only).
 ypred <- predict(svm_fit, Test_Data[[1]])</pre>
 conf_mat <- table(predict = ypred, truth = Test_Data[[2]])</pre>
 corr_pred <- 0
 incorr_pred <- 0</pre>
 for(i in 1:ncol(conf_mat)){
   for(j in 1:ncol(conf_mat)){
     if(j == i){
       corr_pred <- corr_pred + conf_mat[i,j]</pre>
     }
     else
       incorr_pred <- incorr_pred + conf_mat[i,j]</pre>
 Total_MissClass_Rate <- corr_pred/(corr_pred + incorr_pred)
 cat("The accuracy of our model is:", Total_MissClass_Rate)
 ## The accuracy of our model is: 0.9840764
8. Display the confusion matrix.
 conf_mat
           truth
 ## predict 0 1 2
          0 100 0 3
          1 0 116 1
          2 0 1 93
9. Compare the results using the classification method of your
choice (e.g. CNN).
 library(keras)
 # Load the MNIST dataset
 mnist <- dataset_mnist()</pre>
 x_train <- mnist$train$x</pre>
 y_train <- mnist$train$y</pre>
 x_test <- mnist$test$x</pre>
 y_test <- mnist$test$y</pre>
 # Preprocess the data
 x_train <- array_reshape(x_train, c(nrow(x_train), 28, 28, 1))</pre>
 x_test <- array_reshape(x_test, c(nrow(x_test), 28, 28, 1))</pre>
 x_train <- x_train / 255
 x_test <- x_test / 255
 y_train <- to_categorical(y_train, 10)</pre>
 y_test <- to_categorical(y_test, 10)</pre>
 # Define the CNN model architecture
 model <- keras_model_sequential() %>%
   layer_conv_2d(filters = 32, kernel_size = c(3, 3), activation = 'relu',
                input_shape = c(28, 28, 1)) \%
   layer_max_pooling_2d(pool_size = c(2, 2)) %>%
   layer_conv_2d(filters = 64, kernel_size = c(3, 3), activation = 'relu') %>%
   layer_max_pooling_2d(pool_size = c(2, 2)) %>%
   layer_flatten() %>%
   layer_dense(units = 128, activation = 'relu') %>%
   layer_dropout(rate = 0.5) %>%
   layer_dense(units = 10, activation = 'softmax')
 # Compile the model
 model %>% compile(
  loss = 'categorical_crossentropy',
   optimizer = optimizer_rmsprop(),
   metrics = c('accuracy')
 # Train the model
 history <- model %>% fit(
   x_train, y_train,
   epochs = 5,
   batch_size = 128,
   validation_split = 0.2
 ## Epoch 1/5
 ## 375/375 - 15s - loss: 0.3148 - accuracy: 0.9032 - val_loss: 0.0771 - val_accuracy: 0.9786 - 1
 5s/epoch - 40ms/step
 ## Epoch 2/5
 ## 375/375 - 15s - loss: 0.0972 - accuracy: 0.9718 - val_loss: 0.0504 - val_accuracy: 0.9852 - 1
 5s/epoch - 39ms/step
 ## Epoch 3/5
 ## 375/375 - 14s - loss: 0.0678 - accuracy: 0.9803 - val_loss: 0.0418 - val_accuracy: 0.9880 - 1
 4s/epoch - 37ms/step
 ## Epoch 4/5
 ## 375/375 - 15s - loss: 0.0551 - accuracy: 0.9831 - val_loss: 0.0403 - val_accuracy: 0.9883 - 1
 5s/epoch - 39ms/step
 ## Epoch 5/5
 ## 375/375 - 14s - loss: 0.0461 - accuracy: 0.9861 - val_loss: 0.0378 - val_accuracy: 0.9891 - 1
 4s/epoch - 37ms/step
 # Evaluate the model
 score <- model %>% evaluate(x_test, y_test, verbose = 0)
 cat('Test loss:', score[[1]], '\n')
 ## Test loss: 0.02786614
 cat('Test accuracy:', score[[2]], '\n')
 ## Test accuracy: 0.9915
As we can see, the Accuracy for a Convolutional Neural Network is nearly 99% for 10 classes.
10. Test the performance of the SVM by considering other classes
(more difficult to distinguish a priori and by increasing their
numbers). You can also compare your results with another
classifier.
 #results <- benchmarkValues(images.train, labels.train, images.test, labels.test, 10)</pre>
 results <- c(0.9901961, 0.9799073, 0.9904306, 0.9822485, 0.9814815, 0.9812613, 0.9792244, 0.9784
 444, 0.9798000) # I stored the original results to avoid computing them again
 results <- results[2:length(results)]</pre>
 x < -c(2:9)
 Graph_Data <- as.data.frame(cbind(x,results))</pre>
 ggplot(Graph_Data, aes(x, results)) +
   geom_point(col = "blue") +
   scale_x_continuous(breaks = 2:9) +
   labs(title = "The accuracy of SVM model for a given classes (\{0, \ldots, x\})") +
   theme_minimal()
       The accuracy of SVM model for a given classes (\{0, ..., x\})
   0.990
   0.987
   0.981
   0.978
 data_size <- c(2000, 5500, 9000, 12500, 16000, 19500, 23000, 26500, 30000)
 data_size <- 1 - (data_size * 1/60000)
 data_size_scale <- data_size * results
 Graph_Data_rescale <- as.data.frame(cbind(x, data_size_scale))</pre>
 long_title <- "The accuracy of SVM model for a given classes (\{0, \ldots, x\}), rescaled by the frac
 tion of data used to train said model."
 wrapped_title <- str_wrap(long_title, width = 80) # Adjust the width as needed</pre>
 ggplot(Graph_Data_rescale, aes(x, data_size_scale)) +
   geom_point(col = "maroon") +
   scale_x_continuous(breaks = 2:9) +
   labs(title = wrapped_title) +
   theme_minimal()
     The accuracy of SVM model for a given classes ({0, ..., x}), rescaled by the
     fraction of data used to train said model.
   0.5
11. Using the pacakges foreach and doMC (you can consult the
related vignettes foreach or doMC) parallelize the calibration step
by K-fold cross-validation of the parameters \gamma and cost of the
SVM. We will take for example \gamma = cost = 10^{-3:3} and K=5.
In python, the [multiprocessing] module
(https://docs.python.org/2/library/multiprocessing.html), and in
particular the Pool class (with its associated methods, .apply,
.map).
 #For the time purposes I have decided to include only 10% of the data in our Cross-Validation wi
 th all 10 classes. Moreover based on previous results I have assumed that cost must be greater o
 r equal than 10 and that gamma has to be less or equal than 0.1. Hence I have decided to do 3 va
 lues for cost (10, 100, 1000) and 3 for gamma (0.001, 0.01, 0.1).
 Test_Prep <- dataPrep(0.1, 10, images.test, labels.test)</pre>
 Test_Data <- createMatrix(Test_Prep)</pre>
 Train_Prep <- dataPrep(0.1, 10, images.train, labels.train)</pre>
 Train_Data <- createMatrix(Train_Prep)</pre>
 library(e1071)
 library(foreach)
 library(doParallel)
 # Combine predictor variables and response variable into a data frame
 df <- data.frame(Train_Data[[1]], y = Train_Data[[2]])</pre>
 #rm(list=setdiff(ls(), "df"))
 # Define the tuning control (e.g., cross-validation)
 tc <- tune.control(cross = 2) # 5-fold cross-validation</pre>
 # Define the range of values for the cost and gamma parameters
 cost_range <- c(10, 100, 1000)
 gamma_range <- c(0.001, 0.01, 0.1)
 # Define the number of cores for parallel processing
 num_cores <- detectCores() - 1 # Use all available cores except one for the OS</pre>
 # Register parallel backend
 registerDoParallel(cores = num_cores)
 # Perform hyperparameter tuning in parallel
 tune.out <- foreach(cost = cost_range, .combine = rbind) %:%</pre>
   foreach(gamma = gamma_range, .combine = rbind) %dopar% {
     # Perform hyperparameter tuning for the current combination of cost and gamma
     tune_results <- tune(svm, y \sim ., data = df,
                          kernel = "radial", ranges = list(cost = cost, gamma = gamma),
                          tunecontrol = tc)
     cv_accuracy <- 1 - tune_results$best.performance</pre>
     # Return the cost, gamma, and cross-validated accuracy
     c(cost = cost, gamma = gamma, cv_accuracy = cv_accuracy)
 # Stop parallel backend
 stopImplicitCluster()
 # Print the results
 print(tune.out)
            cost gamma cv_accuracy
 ## result.1 10 0.001 0.9160000
 ## result.2 10 0.010 0.9435000
 ## result.3 10 0.100 0.8133333
 ## result.1 100 0.001 0.9155000
 ## result.2 100 0.010 0.9391667
 ## result.3 100 0.100 0.8155000
 ## result.1 1000 0.001 0.9153333
 ## result.2 1000 0.010 0.9448333
 ## result.3 1000 0.100
                         0.8085000
 #Define colors
 custom_colors <- c("maroon", "#FFD700", "darkgreen")</pre>
 # Create the plot
 ggplot(tune.out, aes(x = cost, y = cv_accuracy, color = factor(gamma), group = factor(gamma))) +
   geom_point(size = 3) +
   scale_color_manual(values = custom_colors) +
   scale_x_log10() + # Use log scale for the x-axis (cost)
   labs(title = "Cross-validated Accuracy vs. Cost (with different gamma values)",
        x = "Cost", y = "Cross-validated Accuracy") +
   theme_minimal()
      Cross-validated Accuracy vs. Cost (with different gamma values)
Cross-validated Accuracy
                                                                  factor(gamma)
                                                                   • 0.001
                                                                   0.01
                                                                   • 0.1
        10
                                                           1000
                                 Cost
 ggplot(tune.out, aes(x = gamma, y = cv_accuracy, color = factor(cost), group = factor(cost))) +
   geom_point(size = 3) +
   scale_x_log10() + # Use log scale for the x-axis (cost)
   scale_color_manual(values = custom_colors)+
   labs(title = "Cross-validated Accuracy vs. Cost (with different gamma values)",
        x = "Cost", y = "Cross-validated Accuracy") +
   theme_minimal()
      Cross-validated Accuracy vs. Cost (with different gamma values)
   0.95
Cross-validated Accuracy
                                                                    factor(cost)
                                                                               As we can see, the
                                                                     0 100
       0.001
                                  0.010
                                                             0.100
                                  Cost
best result is obtained for cost = 1000 and gamma = 0.01. Moreover we can observe, that cost plays
little role compared to gamma. Let us now apply that knowledge to a model trained on half of the original
data set and compare it with results from subpoint 10.
 Test_Prep <- dataPrep(0.5, 10, images.test, labels.test)</pre>
 Test_Data <- createMatrix(Test_Prep)</pre>
 Train_Prep <- dataPrep(0.5, 10, images.train, labels.train)</pre>
 Train_Data <- createMatrix(Train_Prep)</pre>
 new_model_results <- fitAndTest(Train_Data, Test_Data, cost_in = 1000, gamma_in = 0.01) #Optimal</pre>
 rization
 old_model_results <- fitAndTest(Train_Data, Test_Data, cost_in = 1, gamma_in = 0.05) #Oryginal p
 arametrization
 c(new_model_results, old_model_results)
 ## [1] 0.9794 0.9772
As we can see, the results for the model indicated by cross validation is doing slightly better than the old
model. We may explain it as a very small difference in gamma, which seems to be the leading
parameter here (as shown on the figures).
```

##

##

0.9

8.0

0.6

Lab 5: MNIST/FMNIST

The homework consists of questions to be solved using R or python commands. You can choose between lab 4 and lab 5. You will type the necessary commands to solve the questions and the

name TML_yourname. Your homework is to be sent via EPI before Monday February 26, 5pm

necessary comments to understand your calculations in a pdf/html file that you will save under the

Homework (lab 4 or lab 5)

2024-02-25

(before class).

}